

APPENDIX

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/* final_x.c - final version of program */
#include <stdio.h>
#include <string.h>
#include <math.h>
#define NO_SEQ      500  /* max number of sequences */
#define NO_AA_SEG 50    /* max sequence length times 10 */

char garbage[40];
FILE *fp, *fo;

void ReadIn_Garbage(int y){
    int x;
    for (x=0; x<y; x++)
        fscanf(fp, "%s", garbage);
}

double factorial(float number){
    /* Good for values less than 170 */
    float gamma[101]={1.000, 99.433, 49.442, 32.785, 24.461,
19.470, 16.146,
13.774, 11.997, 10.616, 9.514, 8.613, 7.863, 7.230,
6.689, 6.220,
5.811, 5.451, 5.132, 4.847, 4.591, 4.360, 4.150, 3.960,
3.786,
3.626, 3.478, 3.343, 3.217, 3.100, 2.992, 2.890, 2.796,
2.707,
2.624, 2.546, 2.473, 2.404, 2.338, 2.277, 2.218, 2.163,
2.110,
2.061, 2.013, 1.968, 1.925, 1.884, 1.845, 1.808, 1.772,
1.738,
1.706, 1.675, 1.645, 1.616, 1.589, 1.562, 1.537, 1.513,
1.489,
1.467, 1.445, 1.424, 1.404, 1.385, 1.366, 1.348, 1.331,
1.314,
1.298, 1.282, 1.267, 1.253, 1.239, 1.225, 1.212, 1.200,
1.187,
1.176, 1.164, 1.153, 1.142, 1.132, 1.122, 1.112, 1.103,
1.094,
1.085, 1.077, 1.069, 1.061, 1.053, 1.046, 1.038, 1.031,
1.025,
1.018, 1.012, 1.006, 1.000};
    double value;
    float t;
    int y;

    if (number > 20.0)
        value = exp(number*log(number)-number +
0.5*log(2*3.14159265*number));
    else if (number == 0.0)
        value = 1.0;
    else {
        value = 1.0;
        t = number;
    }
}
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        while (t > 1.0){
            value = value * t;
            t=t-1.0;
        }
        y=t*100;
        value = value * gamma[y] * t;
    }
    return (value);
}

double Calc_Value(int *root, int *fix, int *root_rand, int *fix_rand)
/* Function that calculates K1 */
{
    float mean[26]={0.072658, 0.000114, 0.024692, 0.050007,
0.061087,
0.041774, 0.071589, 0.023392, 0.052691, 0.000000,
0.063923,
0.089093, 0.023150, 0.042931, 0.000000, 0.052228,
0.039871,
0.052012, 0.073087, 0.055606, 0.000000, 0.063321,
0.012720,
0.000995, 0.032955, 0.000103};
    double K1=0.0, dEnergy, dEnergy_rand;
    int i;
    float th_root, th_fix;
    int total_fix=0, total_root=0;
    float th_root_rand, th_fix_rand;
    float total_fix_rand=0.0, total_root_rand=0.0;
    double K1_rand=0.0;

    for (i=0; i<26; i++){
        total_root+=root[i];
        total_fix+=fix[i];
        total_root_rand+=root_rand[i];
        total_fix_rand+=fix_rand[i];
    }

    for (i=0; i<26; i++){
        /* Calculates Regular Part */
        if (total_fix != 0)
            th_fix = 274.0*fix[i]/total_fix;
        else
            th_fix = 0.0;

        if (total_root != 0)
            th_root = 274.0*root[i]/total_root;
        else
            th_root = 0.0;
        dEnergy=0.0;

        if (mean[i] > 0.001){
            dEnergy=dEnergy+(th_root-th_fix)*log(mean[i])+
                (th_fix-th_root)*log(1-mean[i]);

            if (th_fix > 0.01)
                if (th_fix > 170.0)

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int no_rows;
int  aaname, aanum;
    int s,z,x,y=0;
    int pno=0, mlen, len, fix,no;
    float shit;
int sel, seqflag[500];
char tempc[10];
int atom_pdb,aa_pdb;
int aa_dist[26];
int aa_dist_fix[26];
char sain[20];
char pdbin[20];
int before, after;
int numbers;

printf("Enter structure/alignment file: ");
scanf("%s", sain);
fh=fopen(sain, "r");
fscanf(fh, "%s", pdbin);

/* Sets Up I/O Files */
printf("Enter input filename: ");
scanf("%s", datain);
fp=fopen(datain, "r");
printf("Enter outfile: ");
scanf("%s", dataout);
fo=fopen(dataout, "w");

/* Reads in Header of msf file */

    strcpy(garbage, "duh");
    while (strcmp(garbage, "MSF:"))
        ReadIn_Garbage(1);

    fscanf(fp, "%d", &len);

    while (strcmp(garbage, "Name:"))
        ReadIn_Garbage(1);

/* Calculates mlen and no_rows from len */
    mlen=len/10;
    if (mlen*10 != len)
        mlen++;
    no_rows=mlen/5;
    if (no_rows*5 != mlen)
        no_rows++;
    printf("no_rows = %d ", no_rows);

/* Reads in Sequence names */
    no=0;
    while (strcmp(garbage, "//")){
        fscanf(fp, "%s", seqname[no++]);
        strcpy(garbage, "duh");
        while (strcmp(garbage, "Name:") && strcmp(garbage, "//"))
            ReadIn_Garbage(1);
    }
}

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/* Reads sequence into array */
fscanf(fp, "%s", garbage);
if (strcmp(garbage, "1"))
    numbers=0;
else
    numbers=1;

for (z=0; z<no_rows; z++){
    if (numbers)
        ReadIn_Garbage(2);
    for (y=0; y<no; y++){
        for (x=0; x<5 && 5*z+x < mlen; x++){
            fscanf(fp, "%s", seq[y][(x)+5*(z)]);
            ReadIn_Garbage(1);
        }
    }
}

/* Converts all lowercase to uppercase */

for (z=0; z<len; z++)
    for (y=0; y<no; y++)
        if (seq[y][0][z] >= 'a' && seq[y][0][z] <= 'z')
            seq[y][0][z]=seq[y][0][z]+('A' - 'a');

/* Selection for/against amino acids at a position */
for (x=0; x<2; x++){
    if (x)
        printf("Selection against amino acids (x when
done)\n");
    else
        printf("Selection for amino acids (x when done)\n");
    t=1;
    do {
        printf("Enter amino acid: ");
        scanf("%s", tempc);
        aaname=tempc[0];
        if (aaaname >= 'a' && aaname <= 'z')
            aaname = aaname + ('A' - 'a');
        if (aaaname == 'X' && !x && t) /* Finish that
selection */
            for (y=0; y<no; y++)
                seqflag[y]=1;
        if (aaaname != 'X'){
            printf("Enter amino acid number: ");
            scanf("%d", &aanum);
            for (z=0; z<no; z++)
                if (seq[z][0][aanum-1] == aaname)
                    seqflag[z]=1-x;
        }
        fprintf(fo,"%d - AA=%c, AA#=%d\n", 1-x, aaname,
aanum);
        t=0;
    } while (aaaname != 'X');
}

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        fprintf(fo, "\n");

/* Reads in pdb file */

        fs=fopen(pdbin, "r");
        ft=fopen(strcat(dataout, ".pdb"), "w");

        do{
                fscanf(fs, "%s", garbage);
        } while (strcmp(garbage, "ATOM"));

        x=0;
        do{
                fscanf(fs, "%d", &atom_no[x]);
                fscanf(fs, "%s", atom[x]);
                fscanf(fs, "%s", aa[x]);
                fscanf(fs, "%s", chain[x]);
                fscanf(fs, "%d", &aa_no[x]);
                fscanf(fs, "%f", &pos_x[x]);
                fscanf(fs, "%f", &pos_y[x]);
                fscanf(fs, "%f", &pos_z[x]);
                fscanf(fs, "%f", &occup[x]);
                fscanf(fs, "%f", &B_fac[x++]);
                fscanf(fs, "%s", garbage);
        } while (strcmp(garbage, "END"));
        atom_pdb=x;
        aa_pdb=aa_no[x-1]-aa_no[0]+1;

/* Count amino acids/position */
        for (x=0; x<len; x++){
                for (y=0; y<27; y++){
                        aacount[x][y]=0;
                        aacount_fix[x][y]=0;
                }
                for (x=0; x<m1en; x++){
                        for (z=0; z<10; z++){
                                for (y=0; y<no; y++){
                                        if (seq[y][x][z] >= 'A' && seq[y][x][z] <= 'Z')
                                                aacount[x*10+z][seq[y][x][z]-'A']++;
                                        else if (seq[y][x][z] == '.')
                                                aacount[x*10+z][26]++;
                                        if (seqflag[y]){
                                                if (seq[y][x][z] >= 'A' && seq[y][x][z]
<= 'Z')
                                                        aacount_fix[x*10+z][seq[y][x][z]-
'A']++;
                                                else if (seq[y][x][z] == '.')
                                                        aacount_fix[x*10+z][26]++;
                                        }
                                }
                        }
                }

        temp=0;
        s=0;
        for (x=0; x<26; x++){

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        aa_dist[x]=0;
        aa_dist_fix[x]=0;
    }

    for (x=0; x<26; x++)
        for (y=0; y<len; y++){
            aa_dist[x]+=aaccount[y][x];
            aa_dist_fix[x]+=aaccount_fix[y][x];
        }

    for (y=0; y<aa_pdb; y++){
        if (s>before || y == 0){
            fscanf(fh, "%d", &before);
            if (before || y==0)
                fscanf(fh, "%d", &after);
        }

        if (s == before)
            s = after;

        K1=Calc_Value(aaccount[s], aaccount_fix[s], aa_dist,
aa_dist_fix)/100.0;
        mean_val[y]=K1;
        s++;
    }

    /* Writes filenames to output file */
    for (z=0; z<no_rows; z++){
        for (y=0; y<no; y++){
            if (seqflag[y]){
                fprintf(fo, "%-10s", seqname[y]);
                for (x=0; x<5 && x+5*z!=mlen; x++)
                    fprintf(fo, "%.10s ", seq[y][(x)+(5*z)]);
                fprintf(fo, "\n");
                pno++;
            }
        }
        fprintf(fo, "\n\n");
    }
    printf("no_rows = %d ", no_rows);
    pno=pno/no_rows;

    /* Print AA Composition */
    fix=1;
    do{
        printf("\nAA Comp which position (0 to exit)? ");
        scanf("%d", &fix);
        if (fix != 0){
            for (x=0; x<26; x++) {
                shit=100*aaccount_fix[fix-1][x]/pno;
                printf("%c = %3d (%3.0f%%) ", x+'A',
                    aaccount_fix[fix-1][x], shit);
            }
            shit=100*aaccount_fix[fix-1][26]/pno;
            printf(". = %3d (%3.0f%%)\n", aaccount_fix[fix-
1][26],shit);
        }
    }

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        } while (fix != 0);

temp=0;
s=0;

/* Writes out new PDB file with K1 */
    fprintf(ft, "GRASP PDB FILE\n");
    fprintf(ft, "FORMAT NUMBER=3\n");
    for (y=0; y<atom_pdb; y++){
        if (temp != aa_no[y])
            K1=mean_val[s++];
        fprintf(ft, "ATOM   %4d   %-4s%s %s %3d       %7.3f %7.3f \
%7.3f ", atom_no[y], atom[y], aa[y], chain[y], aa_no[y], pos_x[y],
pos_y[y], pos_z[y]);
        fprintf(ft, " %5f\n", K1);
        temp=aa_no[y];
    }
    fprintf(ft, "END");
}

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/* Reads in pdb */
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do{
    fscanf(fs, "%s", garbage);
} while (strcmp(garbage, "ATOM"));

temp=0;
x=0;
do{
    fscanf(fs, "%d", &atom_no[x]);
    fscanf(fs, "%s", atom[x]);
    fscanf(fs, "%s", aa[x]);
    fscanf(fs, "%s", chain[x]);
    fscanf(fs, "%d", &aa_no[x]);
    fscanf(fs, "%f", &pos_x[x]);
    fscanf(fs, "%f", &pos_y[x]);
    fscanf(fs, "%f", &pos_z[x]);
    fscanf(fs, "%f", &occup[x]);
    fscanf(fs, "%f", &B_fac[x]);

    do{
        fscanf(fs, "%s", garbage);
    }while (strcmp(garbage,"ATOM") && strcmp(garbage, "END"));
    if (temp != aa_no[x])
        temp=aa_no[x++];
    } while (strcmp(garbage, "END"));
atom_pdb=x;
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/* Finds corresponding index for alignment name */
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nameno=-1;
for (i=0; i<no; i++)
    if (!strcmp(seqname[i],searchname))
        nameno=i;
if (nameno == -1)
    printf("Sequence not found!!!!!!\n");

startaa--;

fprintf(fo, "%s\n", datain);
if (startaa !=0)
    fprintf(fo, "0 %d\n", startaa);
x=0;
for (i=startaa; i<len || x<atom_pdb; i++)
    if (seq[nameno][0][i] != '.' && aa_no[x+1] == aa_no[x]+1)
        x++;
    else if (aa_no[x+1] != aa_no[x]+1){
        s=i;
        do {
            x++;
            i++;
        } while (aa_no[x+1] != aa_no[x]+1);
        t=i;
        if (x<atom_pdb)
            fprintf(fo, "%d %d\n", s,t);
    }
    else if (seq[nameno][0][i] == '.'){
```

